



Interest of Human Papillomavirus DNA quantification and genotyping in paired cervical and urine samples to detect cervical lesions

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Background

Cervical cancer is caused by persistent infection with high-risk human papillomavirus (HR-HPV). Conventional human papillomavirus (HPV) testing requires cervical sampling. However, vaginal and urine self-sampling methods are more acceptable for patients and result in increased participation when they are available in screening programs. In this context, we have developed a non-invasive screening method via the detection of HPV DNA in urine samples.

Purpose

To compare HPV viral loads and genotypes in paired cervical and urine samples, and to assess correlation between virological and cytological results in women seeking gynecological consultation.

Methods

Paired urine and cervical specimens were collected and analyzed from 230 of 245 women participating in the previously described prospective PapU study. HPV DNA detection and quantification were performed using a real-time PCR method with short fragment PCR primers. Genotyping was carried out using the INNO-LiPA HPV genotyping assay.

Results

The prevalence of HPV in the 230 paired urine and cervical smear samples was 42 and 49 %, respectively. Overall agreement for HPV positivity and negativity between the paired samples was 90 % ($\kappa = 0.80$). High HPV viral load in both cervical and urine samples was associated with cytological abnormalities. HPV-positive women were mostly infected with HR-HPV types. The agreement between high- and low-risk HPV (LR-HPV) detection in both samples was 97 % ($\kappa = 0.95$ for HR-HPV and $\kappa = 0.97$ for LR-HPV).

Conclusions

High concordance rates for HPV-DNA quantification and high/low-risk HPV genotyping in paired urine/cervical samples suggest that urinary HPV DNA testing could be useful for cervical lesion screening.

Résumé en anglais

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